

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 04:39:04 ; Search time 211.95 Seconds

(without alignments)
3815.365 Million cell updates/sec

Title: US-09-525-361A-23
Perfect score: 471

Sequence: 1 cttgaagattttgtctg.....aactatgagcagtaaat 471

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469.4	99.7	471	21	AA65120
2	469.4	99.7	471	22	AA65500
3	448.4	95.2	480	20	AA65202
4	448.4	95.2	480	21	AA65431
5	448.4	95.2	489	20	AA65704
6	448.4	95.2	489	20	AA65783
7	448.4	95.2	497	20	AA65783
8	448.4	95.2	578	21	AA659470
9	448.4	95.2	578	22	AA657224

10	447	94.9	482	19	AA631992	BS106 polynucleotl
11	447	94.9	482	20	AA63581	BS106 consensus po
12	446.8	94.9	553	19	AA631993	BS106 polynucleotl
13	446.8	94.9	553	20	AA63582	BS106 consensus po
14	446.4	94.8	544	21	AA631765	Human breast speci
15	446.2	94.7	472	22	AA631873	Human BS106 gene-s
16	446.2	94.7	473	22	AA631874	Human BS106 gene-s
17	443	94.1	471	21	AA63509	Membrane-bound pro
18	443	94.1	471	22	AA634245	Human PRO1160 (JUN)
19	442.2	93.9	488	22	AA644870	Human angiotensin
20	442.2	93.9	488	22	AA644870	Human breast cance
21	300.8	63.9	308	19	AA631990	BS106 polynucleotl
22	300.8	63.9	308	20	AA635579	BS106 polynucleotl
23	300.8	63.9	308	22	AA63670	BS106 clone 893988
24	298.8	63.4	501	23	AA637721	Human BS106 gene-s
25	286.8	60.9	292	22	AA631871	DNA encoding novel
26	271.4	57.6	273	21	AA634121	Human BS106 gene-s
27	255.6	54.3	264	22	AA633399	Human BS106 gene-s
28	255.6	54.3	266	22	AA633398	Breast cancer prot
29	247.2	52.5	291	22	AA633397	CDNA encoding SRT
30	202.8	43.1	229	19	AA631989	CDNA encoding SRT
31	202.8	43.1	229	20	AA635578	BS106 polynucleotl
32	186.4	39.6	201	22	AA631866	BS106 clone 166288
33	181.4	38.5	197	19	AA631991	Human BS106 gene-s
34	181.4	38.5	197	20	AA635580	BS106 polynucleotl
35	181.4	38.5	197	20	AA635580	BS106 clone 120981
36	94	20.0	660	23	AA637720	Human BS106 gene-s
37	70.2	14.9	397	20	AA638981	DNA encoding novel
38	65.4	13.9	477	21	AA644307	Splinocebellar at
39	65	13.8	234	16	AA648332	Human SCAT genomic
40	64.8	13.8	1326	23	AA631104	DNA encoding novel
41	64.8	13.8	3376	16	AA631166	AE-9 cDNA. Homo s
42	64.6	13.7	203	19	AA630271	Glutamine rich reg
43	64.6	13.7	203	19	AA631226	SCA2 gene CAG repe
44	64.6	13.7	1037	21	AA639242	Exons E, C and A o
45	64.6	13.7	1472	21	AA639241	Exons D, C, B and

ALIGNMENTS

RESULT 1	AA654120	standard; DNA: 471 BP.
ID	AA654120	
AC	AA654120	
XX		
DT	08-FEB-2001	(first entry)
XX		
DE	Breast cancer protein BCH1 coding sequence.	
KW	Breast cancer; diagnosis; prognosis; detection; screening;	
KW	antibody; oestrogen receptor; anti-oestrogen; immune response;	
KW	lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN2;	
KW	BCN5; BCO2; BCX2; BCX3; BCA2; BCR2; BCT7; BCY3; human; ds.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	47..319
FT		/*tag= a
FT		/product= BCH1 protein
PN	WO200055629-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	15-MAR-2000; 2000WO-US06952.	
XX		
PR	15-MAR-1999; 99US-0268665.	
PR	12-NOV-1999; 99US-0439878.	
PR	12-NOV-1999; 99US-0440370.	
PR	15-NOV-1999; 99US-0440493.	